OIPE

#3 ENTERED

RAW SEQUENCE LISTING DATE: 05/16/2002 p.6
PATENT APPLICATION: US/09/950,041 TIME: 13:06:15

Input Set : A:\DX0724XK1seqlist.txt
Output Set: N:\CRF3\05162002\I950041.raw

```
  3 <110> APPLICANT: Hardiman, Gerard T.
  4       Rock, Fernando L.
  5       Bazan, J. Fernando
  6       Kastelein, Robert A.
  7       Ho, Stephen W.K.
  8       Liu, Yong-Jun
 10 <120> TITLE OF INVENTION: RECEPTOR PROTEINS; RELATED REAGENTS AND METHODS
 12 <130> FILE REFERENCE: DX0724XK1
 14 <140> CURRENT APPLICATION NUMBER: 09/950,041
C--> 15 <141> CURRENT FILING DATE: 2002-05-06
 17 <150> PRIOR APPLICATION NUMBER: 09/728,540
 18 <151> PRIOR FILING DATE: 2000-11-28
 20 <150> PRIOR APPLICATION NUMBER: 60/207,558
 21 <151> PRIOR FILING DATE: 2000-05-25
 23 <150> PRIOR APPLICATION NUMBER: 09/073,363
 24 <151> PRIOR FILING DATE: 1999-06-05
 26 <150> PRIOR APPLICATION NUMBER: 60/044,293
 27 <151> PRIOR FILING DATE: 1997-05-07
 29 <150> PRIOR APPLICATION NUMBER: 60/072,212
 30 <151> PRIOR FILING DATE: 1998-01-22
 32 <150> PRIOR APPLICATION NUMBER: 60/076,947
 33 <151> PRIOR FILING DATE: 1998-03-05
 35 <160> NUMBER OF SEQ ID NOS: 45
 37 <170> SOFTWARE: PatentIn version 3.1
 39 <210> SEQ ID NO: 1
 40 <211> LENGTH: 2367
 41 <212> TYPE: DNA
 42 <213> ORGANISM: Homo sapiens
 44 <220> FEATURE:
 45 <221> NAME/KEY: CDS
 46 <222> LOCATION: (1)..(2358)
 47 <223> OTHER INFORMATION:
 50 <220> FEATURE:
 51 <221> NAME/KEY: mat_peptide
 52 <222> LOCATION: (67)..()
 53 <223> OTHER INFORMATION:
 56 <400> SEQUENCE: 1
 57 atg act agc atc ttc cat ttt gcc att atc ttc atg tta ata ctt cag      48
 58 Met Thr Ser Ile Phe His Phe Ala Ile Ile Phe Met Leu Ile Leu Gln
 59         -20                 -15                 -10
 61 atc aga ata caa tta tct gaa gaa agt gaa ttt tta gtt gat agg tca      96
 62 Ile Arg Ile Gln Leu Ser Glu Glu Ser Glu Phe Leu Val Asp Arg Ser
 63     -5              -1  1               5                  10
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Input Set : **A:\DX0724XKlseqlist.txt**
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65 aaa aac ggt ctc atc cac gtt cct aaa gac cta tcc cag aaa aca aca      144
66 Lys Asn Gly Leu Ile His Val Pro Lys Asp Leu Ser Gln Lys Thr Thr
67                 15                  20                  25
69 atc tta aat ata tcg caa aat tat ata tct gag ctt tgg act tct gac      192
70 Ile Leu Asn Ile Ser Gln Asn Tyr Ile Ser Glu Leu Trp Thr Ser Asp
71             30                  35                  40
73 atc tta tca ctg tca aaa ctg agg att ttg ata att tct cat aat aga      240
74 Ile Leu Ser Leu Ser Lys Leu Arg Ile Leu Ile Ile Ser His Asn Arg
75         45                  50                  55
77 atc cag tat ctt gat atc agt gtt ttc aaa ttc aac cag gaa ttg gaa      288
78 Ile Gln Tyr Leu Asp Ile Ser Val Phe Lys Phe Asn Gln Glu Leu Glu
79     60                  65                  70
81 tac ttg gat ttg tcc cac aac aag ttg gtg aag att tct tgc cac cct      336
82 Tyr Leu Asp Leu Ser His Asn Lys Leu Val Lys Ile Ser Cys His Pro
83 75                  80                  85                  90
85 act gtg aac ctc aag cac ttg gac ctg tca ttt aat gca ttt gat gcc      384
86 Thr Val Asn Leu Lys His Leu Asp Leu Ser Phe Asn Ala Phe Asp Ala
87                 95                  100                 105
89 ctg cct ata tgc aaa gag ttt ggc aat atg tct caa cta aaa ttt ctg      432
90 Leu Pro Ile Cys Lys Glu Phe Gly Asn Met Ser Gln Leu Lys Phe Leu
91             110                 115                 120
93 ggg ttg agc acc aca cac tta gaa aaa tct agt gtg ctg cca att gct      480
94 Gly Leu Ser Thr Thr His Leu Glu Lys Ser Ser Val Leu Pro Ile Ala
95         125                 130                 135
97 cat ttg aat atc agc aag gtc ttg ctg gtc tta gga gag act tat ggg      528
98 His Leu Asn Ile Ser Lys Val Leu Leu Val Leu Gly Glu Thr Tyr Gly
99     140                 145                 150
101 gaa aaa gaa gac cct gag ggc ctt caa gac ttt aac act gag agt ctg      576
102 Glu Lys Glu Asp Pro Glu Gly Leu Gln Asp Phe Asn Thr Glu Ser Leu
103 155                 160                 165                 170
105 cac att gtg ttc ccc aca aac aaa gaa ttc cat ttt att ttg gat gtg      624
106 His Ile Val Phe Pro Thr Asn Lys Glu Phe His Phe Ile Leu Asp Val
107                175                 180                 185
109 tca gtc aag act gta gca aat ctg gaa cta tct aat atc aaa tgt gtg      672
110 Ser Val Lys Thr Val Ala Asn Leu Glu Leu Ser Asn Ile Lys Cys Val
111            190                 195                 200
113 cta gaa gat aac aaa tgt tct tac ttc cta agt att ctg gcg aaa ctt      720
114 Leu Glu Asp Asn Lys Cys Ser Tyr Phe Leu Ser Ile Leu Ala Lys Leu
115        205                 210                 215
117 caa aca aat cca aag tta tca agt ctt acc tta aac aac att gaa aca      768
118 Gln Thr Asn Pro Lys Leu Ser Ser Leu Thr Leu Asn Asn Ile Glu Thr
119     220                 225                 230
121 act tgg aat tct ttc att agg atc ctc caa cta gtt tgg cat aca act      816
122 Thr Trp Asn Ser Phe Ile Arg Ile Leu Gln Leu Val Trp His Thr Thr
123 235                 240                 245                 250
125 gta tgg tat ttc tca att tca aac gtg aag cta cag ggt cag ctg gac      864
126 Val Trp Tyr Phe Ser Ile Ser Asn Val Lys Leu Gln Gly Gln Leu Asp
127                255                 260                 265
129 ttc aga gat ttt gat tat tct ggc act tcc ttg aag gcc ttg tct ata      912
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Input Set : **A:\DX0724XK1seqlist.txt**
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130 Phe Arg Asp Phe Asp Tyr Ser Gly Thr Ser Leu Lys Ala Leu Ser Ile
131             270                 275                 280
133 cac caa gtt gtc agc gat gtg ttc ggt ttt ccg caa agt tat atc tat      960
134 His Gln Val Val Ser Asp Val Phe Gly Phe Pro Gln Ser Tyr Ile Tyr
135         285                 290                 295
137 gaa atc ttt tcg aat atg aac atc aaa aat ttc aca gtg tct ggt aca     1008
138 Glu Ile Phe Ser Asn Met Asn Ile Lys Asn Phe Thr Val Ser Gly Thr
139     300                 305                 310
141 cgc atg gtc cac atg ctt tgc cca tcc aaa att agc ccg ttc ctg cat     1056
142 Arg Met Val His Met Leu Cys Pro Ser Lys Ile Ser Pro Phe Leu His
143 315                 320                 325                 330
145 ttg gat ttt tcc aat aat ctc tta aca gac acg gtt ttt gaa aat tgt     1104
146 Leu Asp Phe Ser Asn Asn Leu Leu Thr Asp Thr Val Phe Glu Asn Cys
147                 335                 340                 345
149 ggg cac ctt act gag ttg gag aca ctt att tta caa atg aat caa tta     1152
150 Gly His Leu Thr Glu Leu Glu Thr Leu Ile Leu Gln Met Asn Gln Leu
151             350                 355                 360
153 aaa gaa ctt tca aaa ata gct gaa atg act aca cag atg aag tct ctg     1200
154 Lys Glu Leu Ser Lys Ile Ala Glu Met Thr Thr Gln Met Lys Ser Leu
155         365                 370                 375
157 caa caa ttg gat att agc cag aat tct gta agc tat gat gaa aag aaa     1248
158 Gln Gln Leu Asp Ile Ser Gln Asn Ser Val Ser Tyr Asp Glu Lys Lys
159     380                 385                 390
161 gga gac tgt tct tgg act aaa agt tta tta agt tta aat atg tct tca     1296
162 Gly Asp Cys Ser Trp Thr Lys Ser Leu Leu Ser Leu Asn Met Ser Ser
163 395                 400                 405                 410
165 aat ata ctt act gac act att ttc aga tgt tta cct ccc agg atc aag     1344
166 Asn Ile Leu Thr Asp Thr Ile Phe Arg Cys Leu Pro Pro Arg Ile Lys
167                 415                 420                 425
169 gta ctt gat ctt cac agc aat aaa ata aag agc att cct aaa caa gtc     1392
170 Val Leu Asp Leu His Ser Asn Lys Ile Lys Ser Ile Pro Lys Gln Val
171             430                 435                 440
173 gta aaa ctg gaa gct ttg caa gaa ctc aat gtt gct ttc aat tct tta     1440
174 Val Lys Leu Glu Ala Leu Gln Glu Leu Asn Val Ala Phe Asn Ser Leu
175         445                 450                 455
177 act gac ctt cct gga tgt ggc agc ttt agc agc ctt tct gta ttg atc     1488
178 Thr Asp Leu Pro Gly Cys Gly Ser Phe Ser Ser Leu Ser Val Leu Ile
179     460                 465                 470
181 att gat cac aat tca gtt tcc cac cca tca gct gat ttc ttc cag agc     1536
182 Ile Asp His Asn Ser Val Ser His Pro Ser Ala Asp Phe Phe Gln Ser
183 475                 480                 485                 490
185 tgc cag aag atg agg tca ata aaa gca ggg gac aat cca ttc caa tgt     1584
186 Cys Gln Lys Met Arg Ser Ile Lys Ala Gly Asp Asn Pro Phe Gln Cys
187                 495                 500                 505
189 acc tgt gag ctc gga gaa ttt gtc aaa aat ata gac caa gta tca agt     1632
190 Thr Cys Glu Leu Gly Glu Phe Val Lys Asn Ile Asp Gln Val Ser Ser
191             510                 515                 520
193 gaa gtg tta gag ggc tgg cct gat tct tat aag tgt gac tac ccg gaa     1680
194 Glu Val Leu Glu Gly Trp Pro Asp Ser Tyr Lys Cys Asp Tyr Pro Glu
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Input Set : **A:\DX0724XK1seqlist.txt**
Output Set: **N:\CRF3\05162002\I950041.raw**

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195         525                 530                 535
197 agt tat aga gga acc cta cta aag gac ttt cac atg tct gaa tta tcc     1728
198 Ser Tyr Arg Gly Thr Leu Leu Lys Asp Phe His Met Ser Glu Leu Ser
199     540                 545                 550
201 tgc aac ata act ctg ctg atc gtc acc atc gtt gcc acc atg ctg gtg     1776
202 Cys Asn Ile Thr Leu Leu Ile Val Thr Ile Val Ala Thr Met Leu Val
203 555                 560                 565                 570
205 ttg gct gtg act gtg acc tcc ctc tgc atc tac ttg gat ctg ccc tgg     1824
206 Leu Ala Val Thr Val Thr Ser Leu Cys Ile Tyr Leu Asp Leu Pro Trp
207                 575                 580                 585
209 tat ctc agg atg gtg tgc cag tgg acc cag acc cgg cgc agg gcc agg     1872
210 Tyr Leu Arg Met Val Cys Gln Trp Thr Gln Thr Arg Arg Arg Ala Arg
211             590                 595                 600
213 aac ata ccc tta gaa gaa ctc caa aga aat ctc cag ttt cat gca ttt     1920
214 Asn Ile Pro Leu Glu Glu Leu Gln Arg Asn Leu Gln Phe His Ala Phe
215         605                 610                 615
217 att tca tat agt ggg cac gat tct ttc tgg gtg aag aat gaa tta ttg     1968
218 Ile Ser Tyr Ser Gly His Asp Ser Phe Trp Val Lys Asn Glu Leu Leu
219     620                 625                 630
221 cca aac cta gag aaa gaa ggt atg cag att tgc ctt cat gag aga aac     2016
222 Pro Asn Leu Glu Lys Glu Gly Met Gln Ile Cys Leu His Glu Arg Asn
223 635                 640                 645                 650
225 ttt gtt cct ggc aag agc att gtg gaa aat atc atc acc tgc att gag     2064
226 Phe Val Pro Gly Lys Ser Ile Val Glu Asn Ile Ile Thr Cys Ile Glu
227                 655                 660                 665
229 aag agt tac aag tcc atc ttt gtt ttg tct ccc aac ttt gtc cag agt     2112
230 Lys Ser Tyr Lys Ser Ile Phe Val Leu Ser Pro Asn Phe Val Gln Ser
231             670                 675                 680
233 gaa tgg tgc cat tat gaa ctc tac ttt gcc cat cac aat ctc ttt cat     2160
234 Glu Trp Cys His Tyr Glu Leu Tyr Phe Ala His His Asn Leu Phe His
235         685                 690                 695
237 gaa gga tct aat agc tta atc ctg atc ttg ctg gaa ccc att ccg cag     2208
238 Glu Gly Ser Asn Ser Leu Ile Leu Ile Leu Leu Glu Pro Ile Pro Gln
239     700                 705                 710
241 tac tcc att cct agc agt tat cac aag ctc aaa agt ctc atg gcc agg     2256
242 Tyr Ser Ile Pro Ser Ser Tyr His Lys Leu Lys Ser Leu Met Ala Arg
243 715                 720                 725                 730
245 agg act tat ttg gaa tgg ccc aag gaa aag agc aaa cgt ggc ctt ttt     2304
246 Arg Thr Tyr Leu Glu Trp Pro Lys Glu Lys Ser Lys Arg Gly Leu Phe
247                 735                 740                 745
249 tgg gct aac tta agg gca gcc att aat att aag ctg aca gag caa gca     2352
250 Trp Ala Asn Leu Arg Ala Ala Ile Asn Ile Lys Leu Thr Glu Gln Ala
251             750                 755                 760
253 aag aaa tagtctaga                                               2367
254 Lys Lys
258 <210> SEQ ID NO: 2
259 <211> LENGTH: 786
260 <212> TYPE: PRT
261 <213> ORGANISM: Homo sapiens
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RAW SEQUENCE LISTING DATE: 05/16/2002
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Input Set : **A:\DX0724XK1seqlist.txt**
Output Set: **N:\CRF3\05162002\I950041.raw**

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263 <400> SEQUENCE: 2
265 Met Thr Ser Ile Phe His Phe Ala Ile Ile Phe Met Leu Ile Leu Gln
266         -20                 -15                 -10
269 Ile Arg Ile Gln Leu Ser Glu Glu Ser Glu Phe Leu Val Asp Arg Ser
270     -5              -1  1               5                   10
273 Lys Asn Gly Leu Ile His Val Pro Lys Asp Leu Ser Gln Lys Thr Thr
274                 15                  20                  25
277 Ile Leu Asn Ile Ser Gln Asn Tyr Ile Ser Glu Leu Trp Thr Ser Asp
278             30                  35                  40
281 Ile Leu Ser Leu Ser Lys Leu Arg Ile Leu Ile Ile Ser His Asn Arg
282         45                  50                  55
285 Ile Gln Tyr Leu Asp Ile Ser Val Phe Lys Phe Asn Gln Glu Leu Glu
286     60                  65                  70
289 Tyr Leu Asp Leu Ser His Asn Lys Leu Val Lys Ile Ser Cys His Pro
290 75                  80                  85                  90
293 Thr Val Asn Leu Lys His Leu Asp Leu Ser Phe Asn Ala Phe Asp Ala
294                 95                  100                 105
297 Leu Pro Ile Cys Lys Glu Phe Gly Asn Met Ser Gln Leu Lys Phe Leu
298             110                 115                 120
301 Gly Leu Ser Thr Thr His Leu Glu Lys Ser Ser Val Leu Pro Ile Ala
302         125                 130                 135
305 His Leu Asn Ile Ser Lys Val Leu Leu Val Leu Gly Glu Thr Tyr Gly
306     140                 145                 150
309 Glu Lys Glu Asp Pro Glu Gly Leu Gln Asp Phe Asn Thr Glu Ser Leu
310 155                 160                 165                 170
313 His Ile Val Phe Pro Thr Asn Lys Glu Phe His Phe Ile Leu Asp Val
314                 175                 180                 185
317 Ser Val Lys Thr Val Ala Asn Leu Glu Leu Ser Asn Ile Lys Cys Val
318             190                 195                 200
321 Leu Glu Asp Asn Lys Cys Ser Tyr Phe Leu Ser Ile Leu Ala Lys Leu
322         205                 210                 215
325 Gln Thr Asn Pro Lys Leu Ser Ser Leu Thr Leu Asn Asn Ile Glu Thr
326     220                 225                 230
329 Thr Trp Asn Ser Phe Ile Arg Ile Leu Gln Leu Val Trp His Thr Thr
330 235                 240                 245                 250
333 Val Trp Tyr Phe Ser Ile Ser Asn Val Lys Leu Gln Gly Gln Leu Asp
334                 255                 260                 265
337 Phe Arg Asp Phe Asp Tyr Ser Gly Thr Ser Leu Lys Ala Leu Ser Ile
338             270                 275                 280
341 His Gln Val Val Ser Asp Val Phe Gly Phe Pro Gln Ser Tyr Ile Tyr
342         285                 290                 295
345 Glu Ile Phe Ser Asn Met Asn Ile Lys Asn Phe Thr Val Ser Gly Thr
346     300                 305                 310
349 Arg Met Val His Met Leu Cys Pro Ser Lys Ile Ser Pro Phe Leu His
350 315                 320                 325                 330
353 Leu Asp Phe Ser Asn Asn Leu Leu Thr Asp Thr Val Phe Glu Asn Cys
354                 335                 340                 345
357 Gly His Leu Thr Glu Leu Glu Thr Leu Ile Leu Gln Met Asn Gln Leu
358             350                 355                 360
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RAW SEQUENCE LISTING ERROR SUMMARY DATE: 05/16/2002
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Input Set : **A:\DX0724XK1seqlist.txt**
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Please Note:
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:17; Xaa Pos. 93,149
Seq#:18; Xaa Pos. 93,149
Seq#:19; Xaa Pos. 48
Seq#:20; Xaa Pos. 48
Seq#:23; N Pos. 316,380,407,408
Seq#:23; Xaa Pos. 35,105,106,127,136
Seq#:24; Xaa Pos. 35,105,106,127,136
Seq#:36; Xaa Pos. 725
Seq#:37; Xaa Pos. 725
Seq#:40; N Pos. 2529

VERIFICATION SUMMARY DATE: 05/16/2002
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Input Set : **A:\DX0724XK1seqlist.txt**
Output Set: **N:\CRF3\05162002\I950041.raw**

L:15 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:2818 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17 after pos.:288
L:2834 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17 after pos.:480
L:2913 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18 after pos.:80
L:2929 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18 after pos.:144
L:2958 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:19 after pos.:144
L:3018 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:20 after pos.:32
L:3191 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23 after pos.:144
L:3206 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23 after pos.:288
L:3207 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23 after pos.:336
L:3210 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23 after pos.:336
L:3211 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23 after pos.:384
L:3214 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23 after pos.:384
L:3215 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23 after pos.:432
L:3299 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:24 after pos.:32
L:3315 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:24 after pos.:96
L:3319 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:24 after pos.:112
L:3323 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:24 after pos.:128
L:4785 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:36 after pos.:2256
L:5057 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:37 after pos.:736
L:5819 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:40 after pos.:2515